

CLAIMS

1. A biopolymer automatic identifying method comprising:

- a mass measurement procedure for measuring the mass of a biopolymer in a sample by mass spectrometry;

- a database search procedure for retrieving a candidate molecule by matching an observed mass value obtained by said mass measurement procedure with a predetermined database;

- a candidate molecule selection procedure for selecting an arbitrary number of candidate molecules with a high similarity score;

- a mass value calibration procedure for calibrating the observed mass value using the candidate molecules as an internal standard;

- a procedure for calculating relative error between a calibrated mass value of a candidate molecule obtained by a previous procedure and a theoretical mass value, and for determining the standard deviation of said relative error;

- a procedure for determining the tolerance of said database search procedure from said standard deviation; and

- a procedure for repeating said database search procedure based on said tolerance.

2. The biopolymer automatic identifying method according to claim 1, wherein said mass value calibration procedure comprises:

- calculating relative error between an observed mass value and a theoretical mass value of a candidate molecule selected in said candidate molecule selection procedure;

- estimating a systematic error of the observed mass value by creating a least square line with respect to a plot of the theoretical mass value and the relative error; and

calibrating the observed mass value by subtracting the systematic error from the entire actual measurement values.

3. An information recording medium in which program information for causing a computer system to carry out the individual procedures making up said biopolymer automatic identifying method according to claim 1 or 2 is stored.